

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/643,801A
Source: 11000 - EFS
Date Processed by STIC: 6-28-05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 06/28/2005

PATENT APPLICATION: US/10/643,801A

TIME: 15:14:22

Input Set : N:\efs\10643801A_efs\RTS0678USSEQ.txt

Output Set: N:\CRF4\06282005\J643801A.raw

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3 <110> APPLICANT: Sanjay Bhanot
4   Kenneth W. Dobie
6 <120> TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
8 <130> FILE REFERENCE: RTS-0678US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/643,801A
C--> 10 <141> CURRENT FILING DATE: 2003-08-18
10 <160> NUMBER OF SEQ ID NOS: 233
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 20
15 <212> TYPE: DNA
16 <213> ORGANISM: Artificial Sequence
18 <220> FEATURE:
20 <223> OTHER INFORMATION: Antisense Oligonucleotide
22 <400> SEQUENCE: 1
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27 <211> LENGTH: 20
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
33 <223> OTHER INFORMATION: Antisense Oligonucleotide
35 <400> SEQUENCE: 2
36 gtgcgcgcga gcccgaaatc                               20
39 <210> SEQ ID NO: 3
40 <211> LENGTH: 20
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
46 <223> OTHER INFORMATION: Antisense Oligonucleotide
48 <400> SEQUENCE: 3
49 atgcattctg cccccaagga                               20
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53 <211> LENGTH: 2439
54 <212> TYPE: DNA
55 <213> ORGANISM: H. sapiens
57 <220> FEATURE:
59 <220> FEATURE:
60 <221> NAME/KEY: CDS
61 <222> LOCATION: (231)...(1397)
63 <400> SEQUENCE: 4
64 ctccgggaac gccagcgccg cggctgccgc ctctgctggg gtctaggctg tttctctcgc   60
66 gccaccactg gccgcgggcc gcagctccag gtgtcctagc cgccagcct cgacgccgtc   120
68 ccgggacccc tgtgtctctgc gcgaagccct ggccccgggg gccggggcat gggccagggg   180

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70 cgcggggtga agcggttcc cgcggggccg tgactgggcg ggcttcagcc atg aag 236
71                                     Met Lys
72                                     1
74 acc ctc ata gcc gcc tac tcc ggg gtc ctg cgc ggc gag cgt cag gcc 284
75 Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu Arg Gln Ala
76         5         10         15
78 gag gct gac cgg agc cag cgc tct cac gga gga cct gcg ctg tcg cgc 332
79 Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro Ala Leu Ser Arg
80         20         25         30
82 gag ggg tct ggg aga tgg ggc act gga tcc agc atc ctc tcc gcc ctc 380
83 Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser Ile Leu Ser Ala Leu
84 35         40         45         50
86 cag gac ctc ttc tct gtc acc tgg ctc aat agg tcc aag gtg gaa aag 428
87 Gln Asp Leu Phe Ser Val Thr Trp Leu Asn Arg Ser Lys Val Glu Lys
88         55         60         65
90 cag cta cag gtc atc tca gtg ctc cag tgg gtc ctg tcc ttc ctt gta 476
91 Gln Leu Gln Val Ile Ser Val Leu Gln Trp Val Leu Ser Phe Leu Val
92         70         75         80
94 ctg gga gtg gcc tgc agt gcc atc ctc atg tac ata ttc tgc act gat 524
95 Leu Gly Val Ala Cys Ser Ala Ile Leu Met Tyr Ile Phe Cys Thr Asp
96         85         90         95
98 tgc tgg ctc atc gct gtg ctc tac ttc act tgg ctg gtg ttt gac tgg 572
99 Cys Trp Leu Ile Ala Val Leu Tyr Phe Thr Trp Leu Val Phe Asp Trp
100 100         105         110
102 aac aca ccc aag aaa ggt ggc agg agg tca cag tgg gtc cga aac tgg 620
103 Asn Thr Pro Lys Lys Gly Gly Arg Arg Ser Gln Trp Val Arg Asn Trp
104 115         120         125         130
106 gct gtg tgg cgc tac ttt cga gac tac ttt ccc atc cag ctg gtg aag 668
107 Ala Val Trp Arg Tyr Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys
108         135         140         145
110 aca cac aac ctg ctg acc acc agg aac tat atc ttt gga tac cac ccc 716
111 Thr His Asn Leu Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro
112         150         155         160
114 cat ggt atc atg ggc ctg ggt gcc ttc tgc aac ttc agc aca gag gcc 764
115 His Gly Ile Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala
116         165         170         175
118 aca gaa gtg agc aag aag ttc cca ggc ata cgg cct tac ctg gct aca 812
119 Thr Glu Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr
120         180         185         190
122 ctg gca ggc aac ttc cga atg cct gtg ttg agg gag tac ctg atg tct 860
123 Leu Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser
124 195         200         205         210
126 gga ggt atc tgc cct gtc agc cgg gac acc ata gac tat ttg ctt tca 908
127 Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu Ser
128         215         220         225
130 aag aat ggg agt ggc aat gct atc atc atc gtg gtc ggg ggt gcg gct 956
131 Lys Asn Gly Ser Gly Asn Ala Ile Ile Val Val Gly Gly Ala Ala
132         230         235         240
134 gag tct ctg agc tcc atg cct ggc aag aat gca gtc acc ctg cgg aac 1004

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135 Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr Leu Arg Asn
136          245          250          255
138 cgc aag ggc ttt gtg aaa ctg gcc ctg cgt cat gga gct gac ctg gtt 1052
139 Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly Ala Asp Leu Val
140      260          265          270
142 ccc atc tac tcc ttt gga gag aat gaa gtg tac aag cag gtg atc ttc 1100
143 Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr Lys Gln Val Ile Phe
144 275          280          285          290
146 gag gag ggc tcc tgg ggc cga tgg gtc cag aag aag ttc cag aaa tac 1148
147 Glu Glu Gly Ser Trp Gly Arg Trp Val Gln Lys Lys Phe Gln Lys Tyr
148          295          300          305
150 att ggt ttc gcc cca tgc atc ttc cat ggt cga ggc ctc ttc tcc tcc 1196
151 Ile Gly Phe Ala Pro Cys Ile Phe His Gly Arg Gly Leu Phe Ser Ser
152          310          315          320
154 gac acc tgg ggg ctg gtg ccc tac tcc aag ccc atc acc act gtt gtg 1244
155 Asp Thr Trp Gly Leu Val Pro Tyr Ser Lys Pro Ile Thr Thr Val Val
156          325          330          335
158 gga gag ccc atc acc atc ccc aag ctg gag cac cca acc cag caa gac 1292
159 Gly Glu Pro Ile Thr Ile Pro Lys Leu Glu His Pro Thr Gln Gln Asp
160          340          345          350
162 atc gac ctg tac cac acc atg tac atg gag gcc ctg gtg aag ctc ttc 1340
163 Ile Asp Leu Tyr His Thr Met Tyr Met Glu Ala Leu Val Lys Leu Phe
164 355          360          365          370
166 gac aag cac aag acc aag ttc ggc ctc ccg gag act gag gtc ctg gag 1388
167 Asp Lys His Lys Thr Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu
168          375          380          385
170 gtg aac tga gccagccttc ggggccaaact ccctggagga accagctgca aatcactttt 1447
171 Val Asn
173 ttgctctgta aattttggaag tgtcatgggt gtctgtgggt tattttaaag aaattataac 1507
175 aatttttgcta aaccattaca atgttaggtc ttttttaaga aggaaaaagt cagtatttca 1567
177 agttcttttca cttccagctt gccctgttct aggtggtggc taaatctggg cctaactctgg 1627
179 gtggctcagc taacctctct tcttcccttc ctgaagtgc aaaggaaact cagtcttctt 1687
181 ggggaagaag gattgccatt agtgacttgg accagttaga tgattcactt tttgccccta 1747
183 ggagtagag gcgaaagcca cttctcatal aagccccttt attgccacta cccacgctc 1807
185 gtctagtcct gaaactgcag gaccagtttc tctgccaaagg ggaggagttg gagagcacag 1867
187 ttgccccgtt gtgtgagggc agtagtaggc atctggaatg ctccagtttg atctcccttc 1927
189 tgccacccct acctaccccc tagtcaactca tatcgagacc tggactggcc tccaggatga 1987
191 ggatgggggt ggcaatgaca ccctgcaggg gaaaggactg ccccccacgc accattgcag 2047
193 ggaggatgcc gccacatga gctaggtgga gtaactgggt tttcttgggt ggctgatgac 2107
195 atggatgcag cacagactca gccttggcct ggagcacatg cttactgggt gcctcagttt 2167
197 accttcccca gatcctagat tctggatgtg aggaagagat ccctcttcag aaggggcctg 2227
199 gccttctgag cagcagatta gttccaaagc aggtggcccc cgaacccaag cctcactttt 2287
201 ctgtgccttc ctgaggggggt tgggcccggg aggaaaccca accctctcct gtgtgttctg 2347
203 ttatctcttg atgagatcat tgcacatgt cagacttttg tatatgcctt gaaaataaat 2407
205 gaaagtgaga atccaaaaaa aaaaaaaaaa aa 2439
208 <210> SEQ ID NO: 5
209 <211> LENGTH: 22
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence

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213 <220> FEATURE:
215 <223> OTHER INFORMATION: PCR Primer
217 <400> SEQUENCE: 5
218 catacggcct tacctggcta ca 22
221 <210> SEQ ID NO: 6
222 <211> LENGTH: 24
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
228 <223> OTHER INFORMATION: PCR Primer
230 <400> SEQUENCE: 6
231 cagacatcag gtactccctc aaca 24
234 <210> SEQ ID NO: 7
235 <211> LENGTH: 22
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
241 <223> OTHER INFORMATION: PCR Probe
243 <400> SEQUENCE: 7
244 tggcaggcaa cttccgaatg cc 22
247 <210> SEQ ID NO: 8
248 <211> LENGTH: 19
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
254 <223> OTHER INFORMATION: PCR Primer
256 <400> SEQUENCE: 8
257 gaaggtgaag gtcggagtc 19
260 <210> SEQ ID NO: 9
261 <211> LENGTH: 20
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
267 <223> OTHER INFORMATION: PCR Primer
269 <400> SEQUENCE: 9
270 gaagatggtg atgggatttc 20
273 <210> SEQ ID NO: 10
274 <211> LENGTH: 20
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
280 <223> OTHER INFORMATION: PCR Probe
282 <400> SEQUENCE: 10
283 caagcttccc gttctcagcc 20
286 <210> SEQ ID NO: 11
287 <211> LENGTH: 2262
288 <212> TYPE: DNA
289 <213> ORGANISM: M. musculus
291 <220> FEATURE:

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294 <221> NAME/KEY: CDS
295 <222> LOCATION: (207)...(1373)
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300 tctcgccctg ctgccgccac ggccctgggcg ctgtccctca gctcccggag ctacagcgca      120
302 agccctggcc ccggcggccg gggcatgggt caggggcgcg gcgtgaggcg gctttctgca      180
304 cgcccgtagc gtgcattggc ttcagc atg aag acc ctc atc gcc gcc tac tcc      233
305 Met Lys Thr Leu Ile Ala Ala Tyr Ser
306 1 5
308 ggg gtc ctg cgg ggt gag cgt cgg gcg gaa gct gcc cgc agc gaa aac      281
309 Gly Val Leu Arg Gly Glu Arg Arg Ala Glu Ala Ala Arg Ser Glu Asn
310 10 15 20 25
312 aag aat aaa gga tct gcc ctg tca cgc gag ggg tct ggg cga tgg ggc      329
313 Lys Asn Lys Gly Ser Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly
314 30 35 40
316 act ggc tcc agc atc ctc tca gcc ctc caa gac atc ttc tct gtc acc      377
317 Thr Gly Ser Ser Ile Leu Ser Ala Leu Gln Asp Ile Phe Ser Val Thr
318 45 50 55
320 tgg ctc aac aga tct aag gtg gaa aaa cag ctg cag gtc atc tca gta      425
321 Trp Leu Asn Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val
322 60 65 70
324 cta caa tgg gtc cta tcc ttc ctg gtg cta gga gtg gcc tgc agt gtc      473
325 Leu Gln Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Val
326 75 80 85
328 atc ctc atg tac acc ttc tgc aca gac tgc tgg ctg ata gct gtg ctc      521
329 Ile Leu Met Tyr Thr Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
330 90 95 100 105
332 tac ttc acc tgg ctg gca ttt gac tgg aac acg ccc aag aaa ggt ggc      569
333 Tyr Phe Thr Trp Leu Ala Phe Asp Trp Asn Thr Pro Lys Lys Gly Gly
334 110 115 120
336 agg aga tcg cag tgg gtg cga aac tgg gcc gtg tgg cgc tac ttc cga      617
337 Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr Phe Arg
338 125 130 135
340 gac tac ttt ccc atc cag ctg gtg aag aca cac aac ctg ctg acc acc      665
341 Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu Leu Thr Thr
342 140 145 150
344 agg aac tat atc ttt gga tac cac ccc cat ggc atc atg ggc ctg ggt      713
345 Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile Met Gly Leu Gly
346 155 160 165
348 gcc ttc tgt aac ttc agc aca gag gct act gaa gtc agc aag aag ttt      761
349 Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu Val Ser Lys Lys Phe
350 170 175 180 185
352 cct ggc ata agg ccc tat ttg gct acg ttg gct ggt aac ttc cgg atg      809
353 Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu Ala Gly Asn Phe Arg Met
354 190 195 200
356 cct gtg ctt cgc gag tac ctg atg tct gga ggc atc tgc cct gtc aac      857
357 Pro Val Leu Arg Glu Tyr Leu Met Ser Gly Gly Ile Cys Pro Val Asn
358 205 210 215

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VERIFICATION SUMMARY

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Input Set : N:\efs\10643801A_efs\RTS0678USSEQ.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1241 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:3831 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3835 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:232
L:3846 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3850 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:233